

Sequence ID	Start	Alignment	End	Organism
		1 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420 440 460 480 500 520 540 560 575		
Query_44111 (+)	1		575	
P03680.1 (+)	1		575	Salasvirus phi29
YP_002004529.1 (+)	1		572	Bacillus phage phi29
WP_247177651.1 (+)	14		586	Escherichia coli
QO90036.1 (+)	1		572	Bacillus phage BSTP4
CAA37450.1 (+)	1		575	Bacillus phage phi29
CAA37451.1 (+)	1		575	Bacillus phage phi29
1XHX_A (+)	1		575	Salasvirus phi29
QRD99831.1 (+)	1		575	Bacillus phage BSTP6
MBS4742027.1 (+)	1		572	Bacillus velezensis
UIS65817.1 (+)	1		572	Bacillus phage Arbo1
NP_040719.1 (+)	1		572	Bacillus phage PZA
QRD99284.1 (+)	1		572	Bacillus phage Whiting18
YP_009910331.1 (+)	1		572	Bacillus phage vB_BveP...
UKM96375.1 (+)	1		572	Bacillus phage TBA3
YP_009910660.1 (+)	1		659	Bacillus phage Gxv1
P19894.1 (+)	1		572	Bacillus phage M2
YP_009910694.1 (+)	1		572	Bacillus phage vB_BsuP...
YP_009910718.1 (+)	1		572	Beecentumtrevirus Nf
NP_690635.1 (+)	1		572	Beecentumtrevirus B103